Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/25 20:02:49

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3084905.sorted.bam -c -nw 400 -hm 3
```

1.2. Alignment

Command line:	/home/luna/Desktop/Software/bwa/bwa mem -t 16 -k 30 -R @RG\tID:Singlecell2022\tLB:Library\tPL:ILLUMINA\tSM:sample_SRR3084905 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3084905.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Aug 25 20:02:48 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3084905.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,182,586
Mapped reads	1,966,971 / 90.12%
Unmapped reads	215,615 / 9.88%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	13,313 / 0.61%
Read min/max/mean length	30 / 76 / 76.21
Duplicated reads (estimated)	102,588 / 4.7%
Duplication rate	4.36%
Clipped reads	767,561 / 35.17%

2.2. ACGT Content

Number/percentage of A's	37,983,797 / 28.45%
Number/percentage of C's	24,205,236 / 18.13%
Number/percentage of T's	42,929,682 / 32.16%
Number/percentage of G's	28,360,480 / 21.24%
Number/percentage of N's	20,100 / 0.02%
GC Percentage	39.38%

2.3. Coverage

Mean	0.0431

Standard Deviation	0.3852

2.4. Mapping Quality

Mean Mapping Quality	46.71

2.5. Mismatches and indels

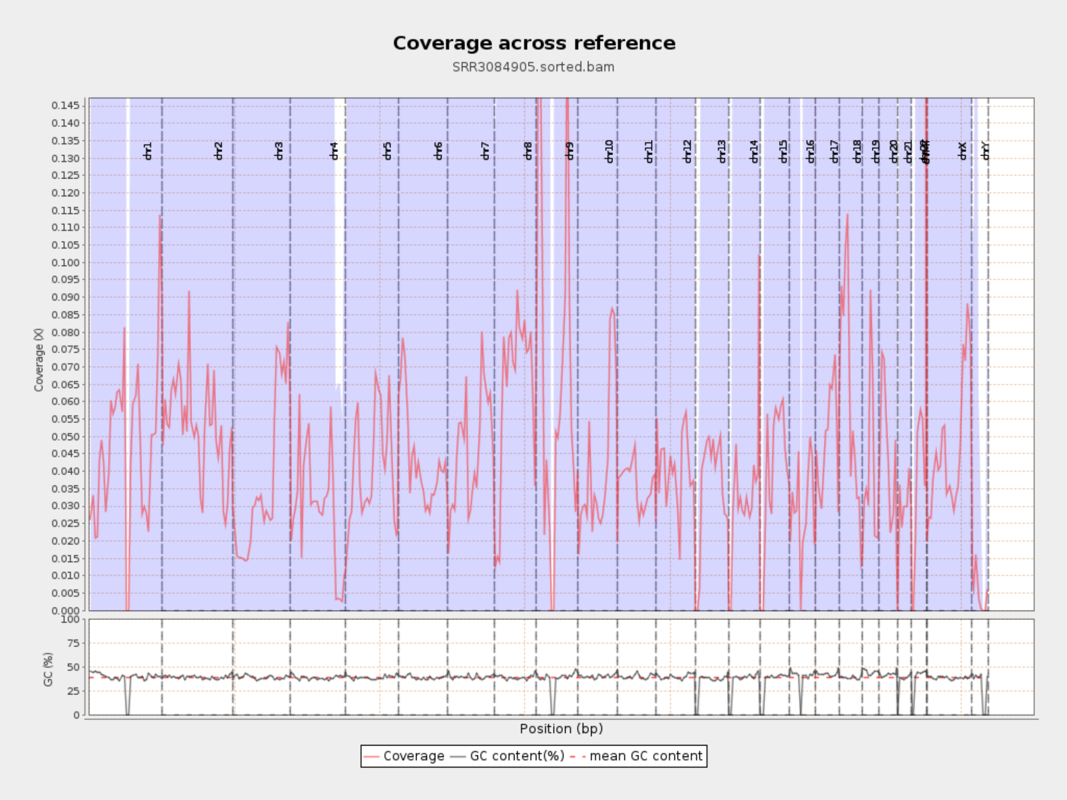
General error rate	0.84%
Mismatches	1,104,543
Insertions	10,564
Mapped reads with at least one insertion	0.53%
Deletions	29,083
Mapped reads with at least one deletion	1.46%
Homopolymer indels	48.74%

2.6. Chromosome stats

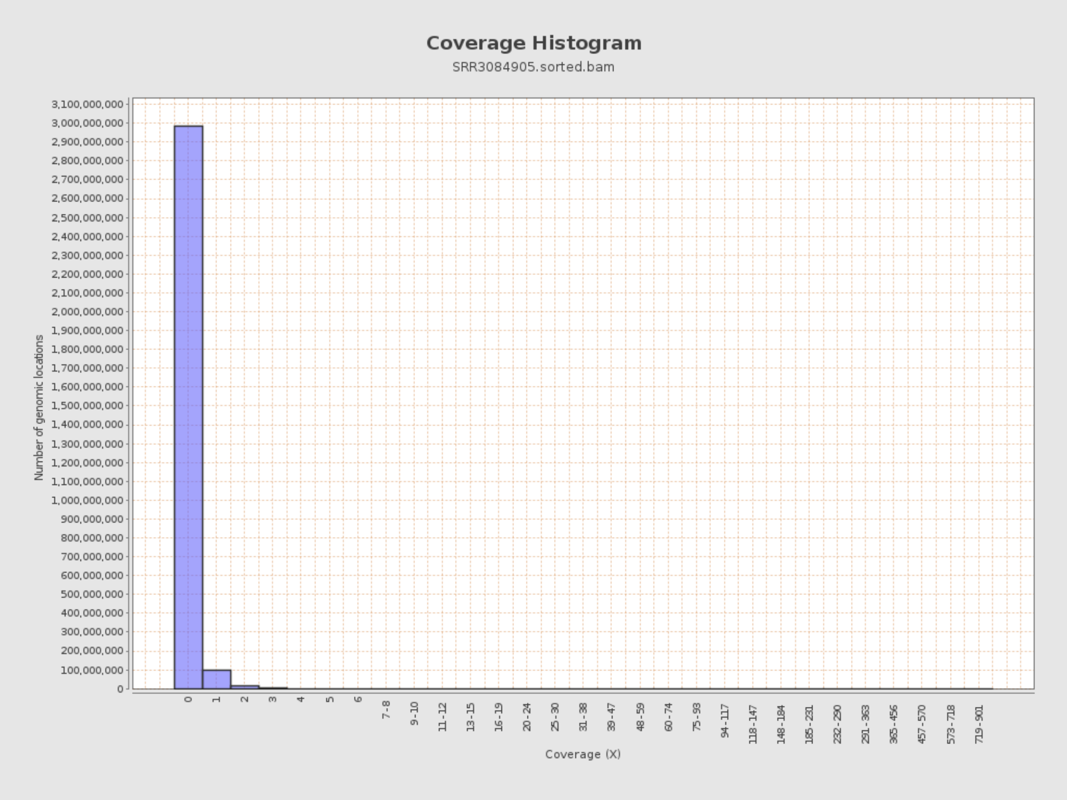
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	11569344	0.0464	0.8094
chr2	243199373	12871270	0.0529	0.4458
chr3	198022430	7306486	0.0369	0.2183
chr4	191154276	5639313	0.0295	0.2062
chr5	180915260	7411467	0.041	0.2384
chr6	171115067	7451955	0.0435	0.2437
chr7	159138663	7433456	0.0467	0.3655

chr8	146364022	9253015	0.0632	0.5315
chr9	141213431	9695838	0.0687	0.4356
chr10	135534747	5605716	0.0414	0.3058
chr11	135006516	4852797	0.0359	0.2647
chr12	133851895	5459124	0.0408	0.2312
chr13	115169878	3986737	0.0346	0.2097
chr14	107349540	3206111	0.0299	0.2079
chr15	102531392	4071689	0.0397	0.2259
chr16	90354753	2683201	0.0297	0.2132
chr17	81195210	4016248	0.0495	0.2552
chr18	78077248	4893447	0.0627	0.6633
chr19	59128983	2452480	0.0415	0.4412
chr20	63025520	2969819	0.0471	0.2532
chr21	48129895	1388725	0.0289	0.2066
chr22	51304566	1769544	0.0345	0.2082
chrMT	16571	94016	5.6735	3.2333
chrX	155270560	7179055	0.0462	0.2609
chrY	59373566	288817	0.0049	0.1153

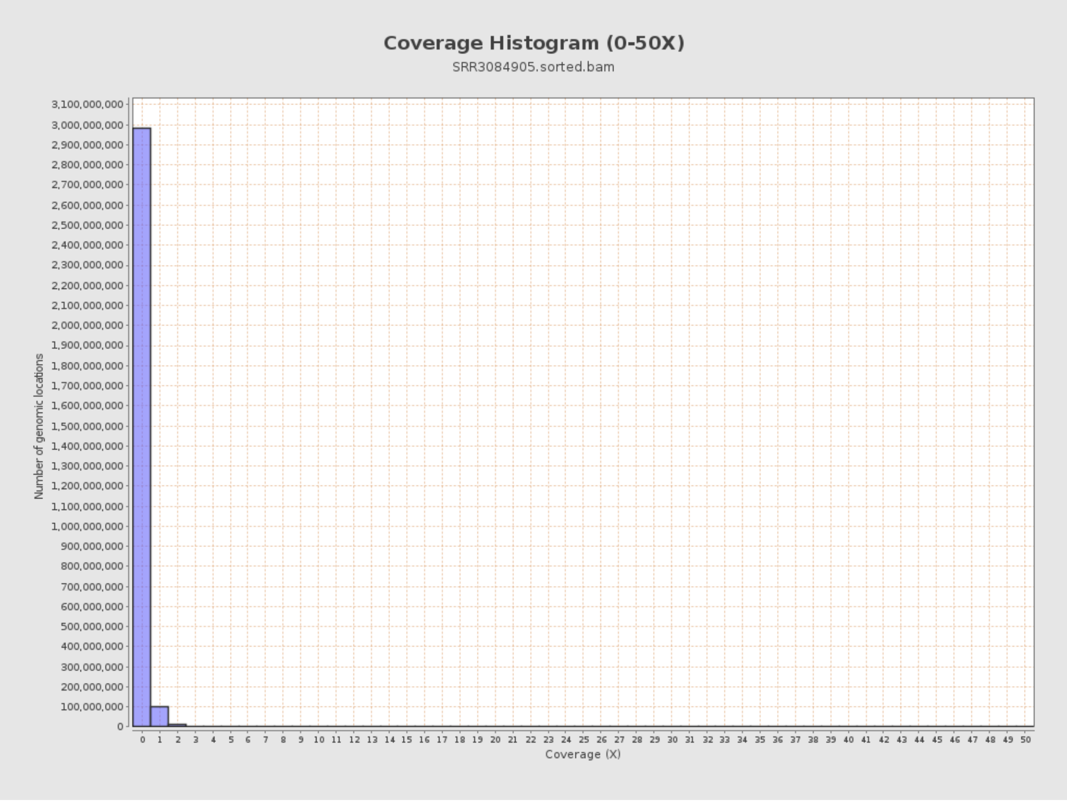
3. Results : Coverage across reference



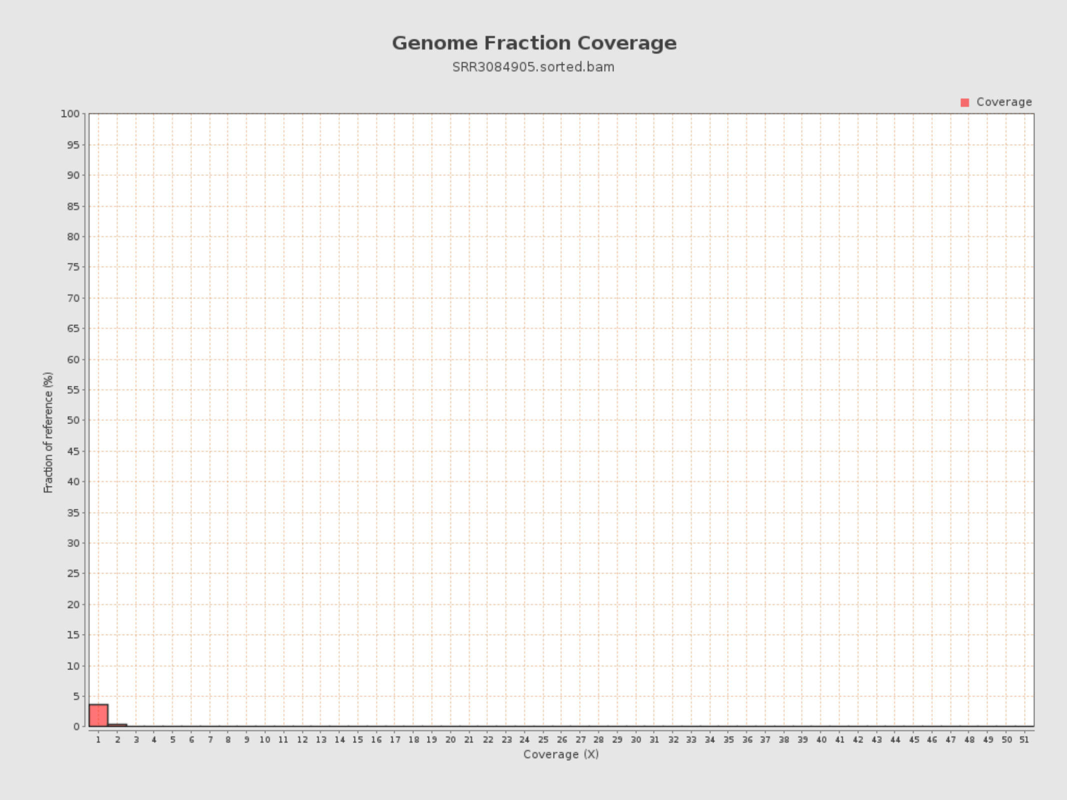
4. Results : Coverage Histogram



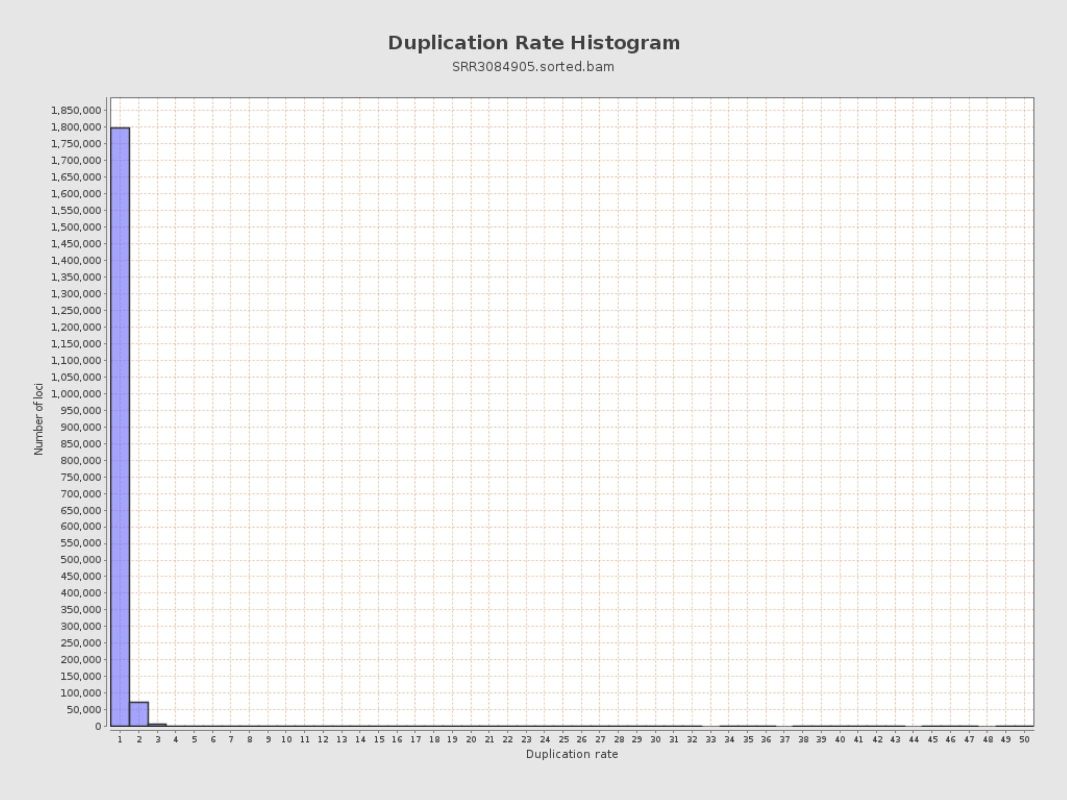
5. Results : Coverage Histogram (0-50X)



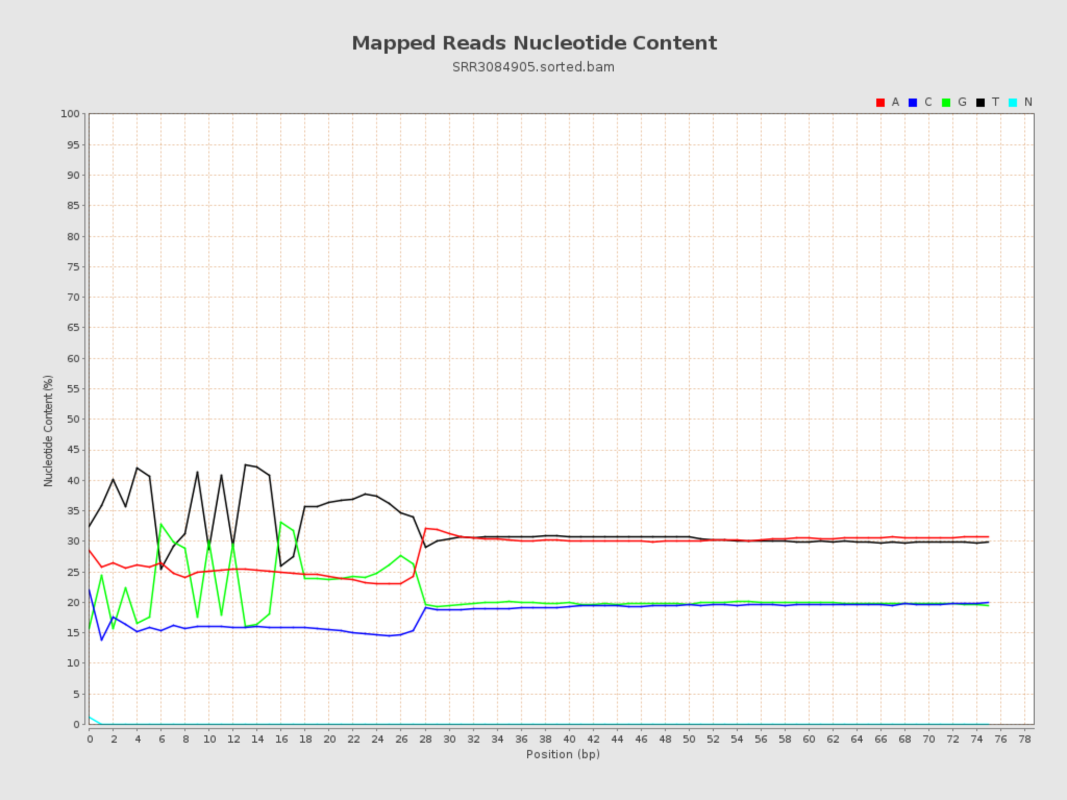
6. Results : Genome Fraction Coverage



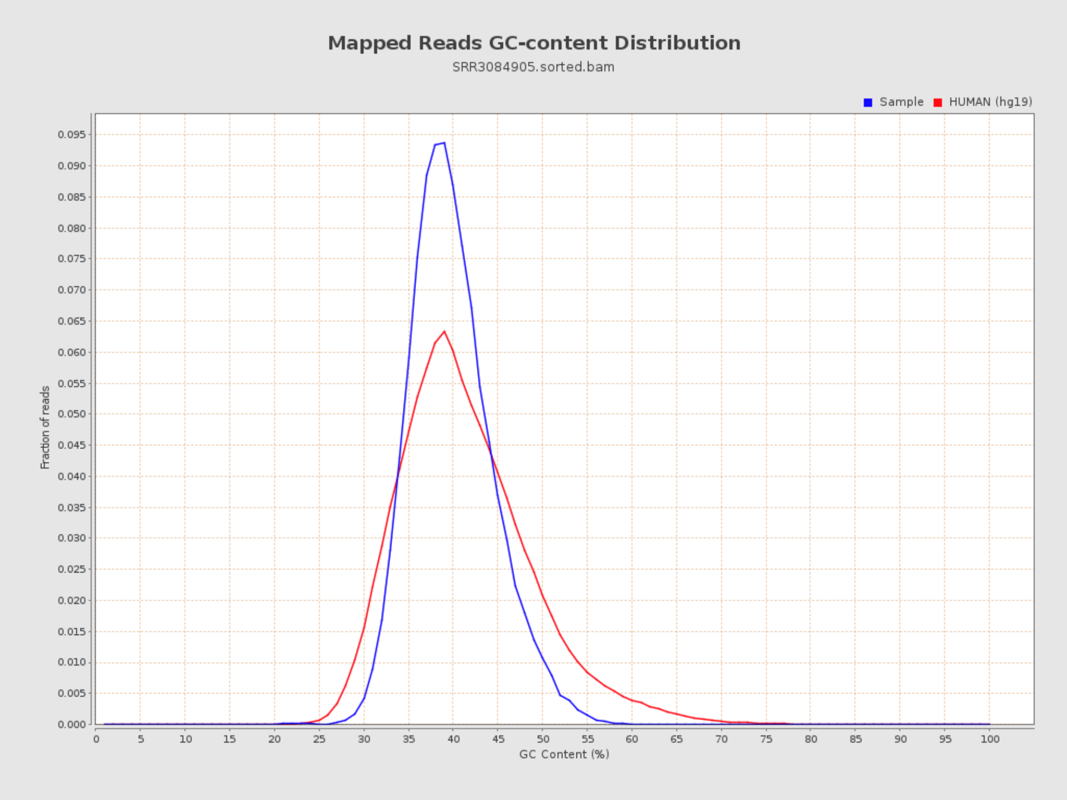
7. Results : Duplication Rate Histogram



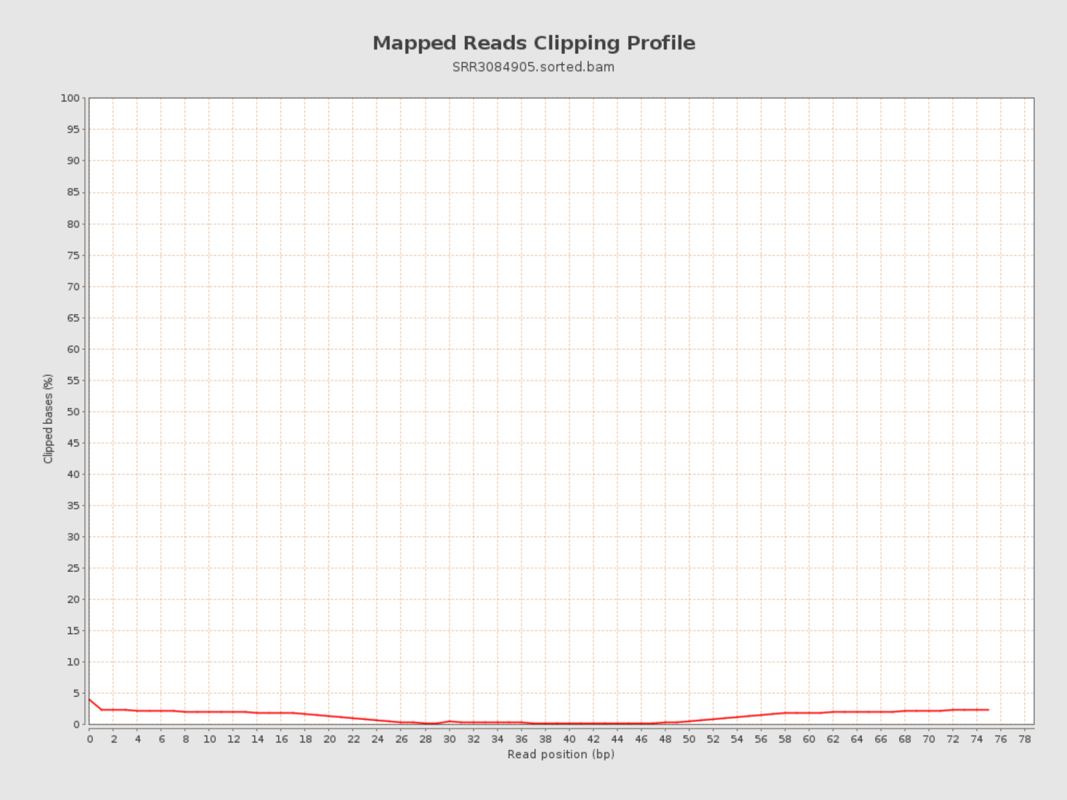
8. Results : Mapped Reads Nucleotide Content



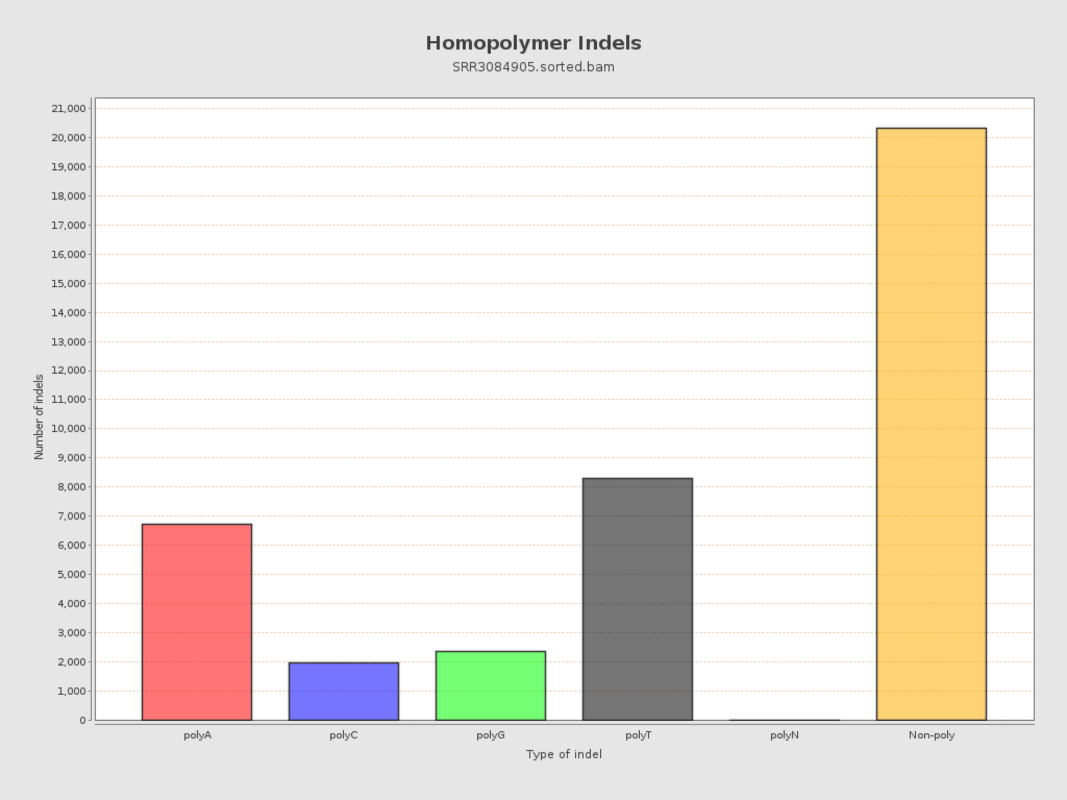
9. Results : Mapped Reads GC-content Distribution



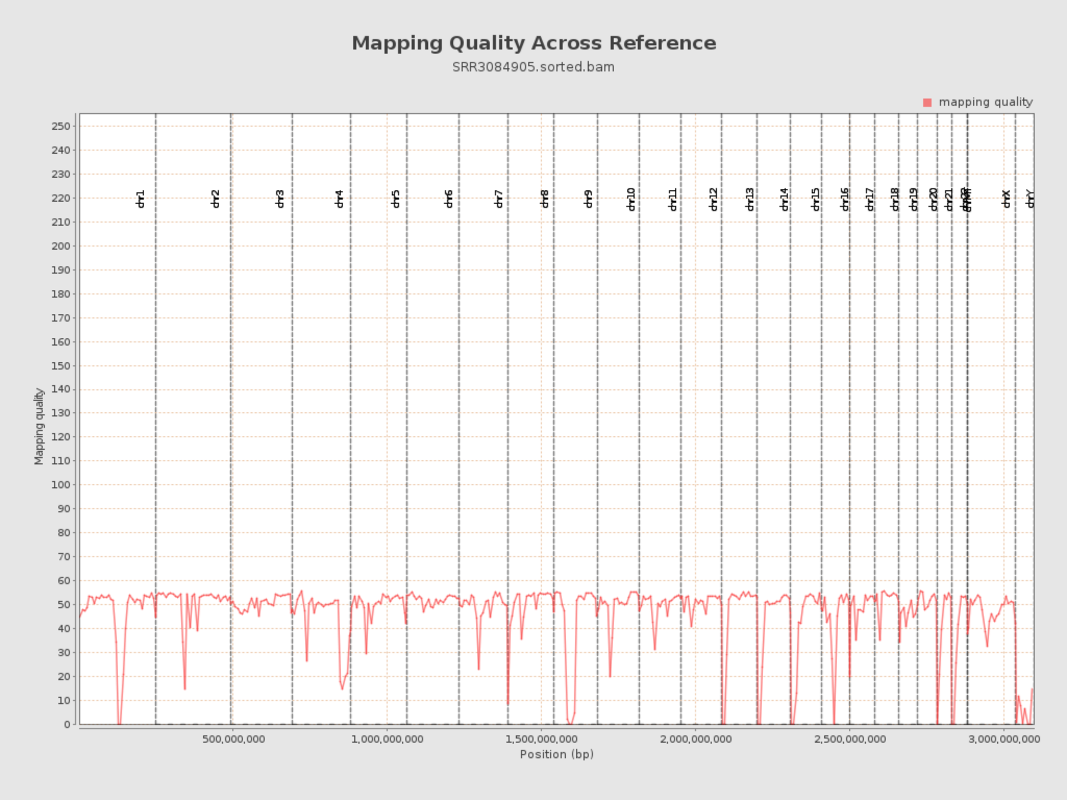
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram